Amendments to the Claims

Please cancel Claims 1-15 and add new Claims 16-130. This listing of claims will replace all prior versions, and listings, of the claims in the application.

Claims 1-15 (Cancelled)

Claim 16. (New) A method for detecting at least one biological entity in a sample, comprising:

(a) combining nucleic acid sequences in a sample with multiple primers of randomized nucleotide sequences, said randomized sequences being sufficiently randomized to provide nonpreferential start sites for amplification of the sample nucleic acid sequences;

(b) performing a plurality of cycles of a polymerase chain reaction to randomly amplify the sample nucleic acid sequences, wherein a detectable nucleoside triphosphate is incorporated during amplification to produce detectable amplification products and wherein sequences corresponding and complementary to only the sample nucleic acid sequences are the amplification products; and,

(c) hybridizing the detectable multiple amplification products to an array of predetermined nucleic acid sequences.

Claim 17. (New) The method of Claim 16, wherein the detectable nucleoside triphosphate is labeled, further comprising detecting the detectable amplification products hybridized to the array.

Claim 18. (New) The method of Claim 17, further comprising relating the detected amplification products to at least one biological entity in the sample.

Claim 19. (New) The method of Claim 16, wherein the primers are four to fifteen nucleotides in length.

Claim 20. (New) The method of Claim 16, wherein the array of predetermined nucleic acid sequences is immobilized on a surface.

Claim 21. (New) The method of Claim 17, wherein the detectable amplification products are enzymatically detected.

Claim 22. (New) The method of Claim 16, wherein the detectable nucleoside triphosphate is biotinylated.

Claim 23. (New) The method of Claim 16, wherein the detectable nucleoside triphosphate is fluorescently labeled.

Claim 24. (New) The method of Claim 16, wherein the detectable nucleoside triphosphate is labeled with digoxigenin.

Claim 25. (New) The method of Claim 16, wherein the detectable nucleoside triphosphate is labeled with radiolabel.

Claim 26. (New) The method of Claim 20, wherein the surface is an opaque membrane.

Claim 27. (New) The method of Claim 20, wherein the surface is silica-based.

Claim 28. (New) The method of Claim 16, wherein the predetermined nucleic acid sequences are at predetermined positions on the array and wherein the nucleic acid sequences at two or more predetermined positions characterize a different biological entity or variant of a biological entity.

Claim 29. (New) The method of Claim 16, wherein the sample comprises multiple biological entities.

Claim 30. (New) The method of Claim 16, wherein the biological entity is a pathogen.

Claim 31. (New) The method of Claim 16, wherein the predetermined nucleic acid sequences are more than 30 nucleotides in length.

Claim 32. (New) A method for detecting at least one biological entity in a sample, comprising:

(a) combining nucleic acid sequences in a sample with multiple primers comprising randomized nucleotide sequences, said randomized sequences being sufficiently randomized to provide amplification products having nucleotide sequences corresponding and complementary to only the sample nucleic acid sequences;

(b) performing a plurality of cycles of a polymerase chain reaction to randomly amplify the sample nucleic acid sequences, wherein a detectable nucleoside triphosphate is incorporated during amplification to produce detectable amplification products; and,

(c) hybridizing the detectable multiple amplification products to an array of predetermined nucleic acid sequences.

Claim 33. (New) The method of Claim 32, further comprising detecting the detectable amplification products hybridized to the array.

Claim 34. (New) The method of Claim 33, further comprising relating the detected amplification products to at least one biological entity in the sample.

Claim 35. (New) The method of Claim 32, wherein the primers are four to fifteen nucleotides in length.

Claim 36. (New) The method of Claim 32, wherein the array of predetermined nucleic acid sequences is immobilized on a surface.

Claim 37. (New) The method of Claim 33, wherein the detectable amplification products are enzymatically detected.

Claim 38. (New) The method of Claim 32, wherein the detectable nucleoside triphosphate is biotinylated.

Claim 39. (New) The method of Claim 32, wherein the detectable nucleoside triphosphate is fluorescently labeled.

Claim 40. (New) The method of Claim 32, wherein the detectable nucleoside triphosphate is labeled with digoxigenin.

Claim 41. (New) The method of Claim 32, wherein the detectable nucleoside triphosphate is labeled with radiolabel.

Claim 42. (New) The method of Claim 36, wherein the surface is an opaque membrane.

Claim 43. (New) The method of Claim 36, wherein the surface is silica-based.

Claim 44. (New) The method of Claim 32, wherein the predetermined nucleic acid sequences are at predetermined positions on the array and wherein the nucleic acid sequences at two or more predetermined positions characterize a different biological entity or variant of a biological entity.

Claim 45. (New) The method of Claim 32, wherein the sample comprises multiple biological entities.

Claim 46. (New) The method of Claim 32, wherein the biological entity is a pathogen.

Claim 47. (New) The method of Claim 32, wherein the predetermined nucleic acid sequences are more than 30 nucleotides in length.

Claim 48. (New) A method for detecting at least one biological entity in a sample, comprising:

(a) combining nucleic acid sequences in a sample with multiple primers comprising randomized nucleotide sequences, said randomized sequences being sufficiently randomized such that substantially all sample nucleic acid sequences are represented among multiple amplification products;

(b) performing a plurality of cycles of a polymerase chain reaction to randomly amplify the sample nucleic acid sequences, wherein a detectable nucleoside triphosphate is incorporated during amplification to produce detectable amplification products and wherein sequences corresponding and complementary to only the sample nucleic acid sequences are the multiple amplification products; and,

(c) hybridizing the labeled multiple amplification products to an array of predetermined nucleic acids.

Claim 49. (New) The method of Claim 48, further comprising detecting the detectable amplification products that hybridized to the array.

Claim 50. (New) The method of Claim 49, further comprising relating the detected amplification products to at least one biological entity in the sample.

Claim 51. (New) The method of Claim 48, wherein the primers are four to fifteen nucleotides in length.

Claim 52. (New) The method of Claim 48, wherein the array of predetermined nucleic acid sequences is immobilized on a surface.

Claim 53. (New) The method of Claim 49, wherein the detectable amplification products are enzymatically detected.

Claim 54. (New) The method of Claim 48, wherein the detectable nucleoside triphosphate is biotinylated.

Claim 55. (New) The method of Claim 48, wherein the detectable nucleoside triphosphate is fluorescently labeled.

Claim 56. (New) The method of Claim 48, wherein the detectable nucleoside triphosphate is labeled with digoxigenin.

Claim 57. (New) The method of Claim 48, wherein the detectable nucleoside triphosphate is labeled with radiolabel.

Claim 58. (New) The method of Claim 52, wherein the surface is an opaque membrane.

Claim 59. (New) The method of Claim 52, wherein the surface is silica-based.

Claim 60. (New) The method of Claim 48, wherein the predetermined nucleic acids are at predetermined positions on the array and wherein the nucleic acid sequences at two or more predetermined positions characterize a different biological entity or variant of a biological entity.

Claim 61. (New) The method of Claim 48, wherein the sample comprises multiple biological entities.

Claim 62. (New) The method of Claim 48, wherein the biological entity is a pathogen.

Claim 63. (New) The method of Claim 48, wherein the predetermined nucleic acid sequences are more than 30 nucleotides in length.

Claim 64. (New) The method of Claim 16, wherein substantially all sample nucleic acid sequences are represented among the multiple amplification products.

Claim 65. (New) The method of Claim 64, further comprising detecting the detectable amplification products that hybridized to the array.

Claim 66. (New) The method of Claim 65, further comprising relating the detected amplification products to at least one biological entity in the sample.

Claim 67. (New) The method of Claim 64, wherein the primers are four to fifteen nucleotides in length.

Claim 68. (New) The method of Claim 64, wherein the array of predetermined nucleic acid sequences is immobilized on a surface.

Claim 69. (New) The method of Claim 65, wherein the detectable amplification products are enzymatically detected.

Claim 70. (New) The method of Claim 64, wherein the detectable nucleoside triphosphate is biotinylated.

Claim 71. (New) The method of Claim 64, wherein the detectable nucleoside triphosphate is fluorescently labeled.

Claim 72. (New) The method of Claim 64, wherein the detectable nucleoside triphosphate is labeled with digoxigenin.

Claim 73. (New) The method of Claim 64, wherein the detectable nucleoside triphosphate is labeled with radiolabel.

Claim 74. (New) The method of Claim 68, wherein the surface is an opaque membrane.

Claim 75. (New) The method of Claim 68, wherein the surface is silica-based.

Claim 76. (New) The method of Claim 64, wherein the predetermined nucleic acids are at predetermined positions on the array and wherein the nucleic acid sequences at two or more predetermined positions characterize a different biological entity or variant of a biological entity.

Claim 77. (New) The method of Claim 64, wherein the sample comprises multiple biological entities.

Claim 78. (New) The method of Claim 64, wherein the biological entity is a pathogen.

Claim 79. (New) The method of Claim 64, wherein the predetermined nucleic acid sequences are more than 30 nucleotides in length.

Claim 80. (New) A method for detecting at least one biological entity in a sample, comprising:

(a) combining nucleic acid sequences in a sample with multiple primers comprising randomized nucleotide sequences, said randomized sequences being sufficiently randomized to provide nonpreferential start sites for amplification of the sample nucleic acid sequences such that substantially all sample nucleic acid sequences are represented among multiple amplification products and said multiple amplification products having nucleotide sequences corresponding and complementary to only the sample nucleic acid sequences;

(b) performing a plurality of cycles of a polymerase chain reaction to randomly amplify the sample nucleic acid sequences at each cycle of the polymerase chain reaction, wherein a detectable nucleoside triphosphate is incorporated during amplification to produce detectable multiple amplification products; and,

(c) hybridizing the labeled multiple amplification products to an array of predetermined nucleic acid sequences.

Claim 81. (New) The method of Claim 80, further comprising detecting the detectable amplification products that hybridized to the array.

Claim 82. (New) The method of Claim 81, further comprising relating the detected amplification products to at least one biological entity in the sample.

Claim 83. (New) The method of Claim 80, wherein the primers are four to fifteen nucleotides in length.

Claim 84. (New) The method of Claim 80, wherein the array of predetermined nucleic acid sequences is immobilized on a surface.

Claim 85. (New) The method of Claim 81, wherein the detectable amplification products are enzymatically detected.

Claim 86. (New) The method of Claim 80, wherein the detectable nucleoside triphosphate is biotinylated.

Claim 87. (New) The method of Claim 80, wherein the detectable nucleoside triphosphate is fluorescently labeled.

Claim 88. (New) The method of Claim 80, wherein the detectable nucleoside triphosphate is labeled with digoxigenin.

Claim 89. (New) The method of Claim 80, wherein the detectable nucleoside triphosphate is labeled with radiolabel.

Claim 90. (New) The method of Claim 84, wherein the surface is an opaque membrane.

Claim 91. (New) The method of Claim 84, wherein the surface is silica-based.

Claim 92. (New) The method of Claim 80, wherein the predetermined nucleic acids are at predetermined positions on the array and wherein the nucleic acid sequences at two or more predetermined positions characterize a different biological entity or variant of a biological entity.

Claim 93. (New) The method of Claim 80, wherein the sample comprises multiple biological entities.

Claim 94. (New) The method of Claim 80, wherein the biological entity is a pathogen.

Claim 95. (New) The method of Claim 80, wherein the predetermined nucleic acid sequences are more than 30 nucleotides in length.

Claim 96. (New) A method for detecting at least one biological entity of a plurality of preselected biological entities potentially present in a sample, comprising:

(a) combining nucleic acid sequences in the sample with multiple primers comprising randomized nucleotide sequences, the randomized sequences being sufficiently randomized to provide nonpreferential start sites for amplification of the sample nucleic acid sequences;

(b) performing a plurality of cycles of a polymerase chain reaction to randomly amplify the sample nucleic acid sequences to produce amplification products; and,

(c) hybridizing the amplification products to an array of predetermined nucleic acid sequences at predetermined positions on the array, wherein the nucleic acid sequences at the predetermined positions characterize at least one of the plurality of preselected biological entities.

Claim 97. (New) The method of Claim 96, wherein the wherein a detectable nucleoside triphosphate is incorporated during amplification to produce detectable multiple amplification products.

Claim 98. (New) The method of Claim 96, wherein the method simultaneously detects two or more biological entities.

Claim 99. (New) The method of Claim 96, wherein the plurality of preselected biological entities is greater than twenty-five.

Claim 100. (New) The method of Claim 96, wherein the plurality of preselected biological entities is greater than fifty.

Claim 101. (New) The method of Claim 96, wherein the plurality of preselected biological entities is greater than one hundred.

Claim 102. (New) The method of Claim 96, wherein the plurality of preselected biological entities is greater than one thousand.

Claim 103. (New) The method of Claim 96, wherein the nucleic acid sequences at the predetermined positions comprise a continuum of highly conserved to highly specific nucleic acids.

Claim 104. (New) The method of Claim 96, wherein the method provides information about the biological entity even if identification of the biological entity cannot be ascertained.

Claim 105. (New) The method of Claim 96, wherein the method provides information on the biological entity including one or more of the following: the kingdom, phylum, class, order, family, genus and species of the biological entity.

Claim 106. (New) The method of Claim 96, wherein the method provides the ability to extract information resident in a genome of the biological entity.

Claim 107. (New) The method of Claim 96, wherein the method provides the ability to extract information about antibiotic resistance of the biological entity.

Claim 108. (New) The method of Claim 96, wherein the method provides the ability to extract information about virulence of the biological entity.

Claim 109. (New) The method of Claim 96, wherein the method provides the ability to extract information about transmissibility of the biological entity.

Claim 110. (New) The method of Claim 96, wherein the method provides the ability to extract information about treatment modalities for the biological entity.

Claim 111. (New) The method of Claim 96, wherein the method detects a genetic alteration in the biological entity.

Claim 112. (New) The method of Claim 96, wherein the method detects an induced genetic alteration in the biological entity.

Claim 113. (New) The method of Claim 96, wherein one or more of the predetermined nucleic acid sequences are redundant on the array.

Claim 114. (New) The method of Claim 96, wherein two or more of the predetermined nucleic acid sequences are overlapping sequences.

Claim 115. (New) The method of Claim 96, wherein two or more of the predetermined nucleic acid sequences are overlapping sequences of a single biological entity.

Claim 116. (New) The method of Claim 96, wherein two or more of the predetermined nucleic acid sequences are sub-sequences of each other.

Claim 117. (New) The method of Claim 96, wherein two or more of the predetermined nucleic acid sequences are nested subset sequences of each other.

Claim 118. (New) The method of Claim 96, wherein the detectable amplification products are hybridized to the array under high stringency conditions.

Claim 119. (New) The method of Claim 96, wherein the detectable amplification products are hybridized to the array under low stringency conditions.

Claim 120. (New) The method of Claim 96, wherein the detectable amplification products are hybridized to the array under hybridization conditions between about 50 and 65 degrees Celsius.

Claim 121. (New) The method of Claim 96, wherein the primers are four to fifteen nucleotides in length.

Claim 122. (New) The method of Claim 96, wherein the primers are four to nine nucleotides in length.

Claim 123. (New) The method of Claim 96, wherein the primers are four to six nucleotides in length.

Claim 124. (New) The method of Claim 96, wherein the primers are greater than six nucleotides in length.

Claim 125. (New) A method for obtaining information resident in a genetic code of at least one biological entity in a sample, comprising:

(a) combining nucleic acid sequences in the sample with multiple primers comprising randomized nucleotide sequences, the randomized sequences being sufficiently randomized to provide nonpreferential start sites for amplification of the sample nucleic acid sequences;

(b) performing a plurality of cycles of a polymerase chain reaction to randomly amplify the sample nucleic acid sequences to produce amplification products; and,

(c) hybridizing the amplification products to an array of predetermined nucleic acid sequences at predetermined positions on the array,

wherein detection of hybridized amplification products on the array provides genetic information about the biological entity.

Claim 126. (New) The method of Claim 125, wherein substantially all sample nucleic acid sequences are represented among the multiple amplification products.

Claim 127. (New) The method of Claim 125, wherein the genetic information characterizes the biological entity.

Claim 128. (New) The method of Claim 125, wherein the genetic information identifies the biological entity.

Claim 129. (New) The method of Claim 125 wherein the genetic information monitors the biological entity.

Claim 130. (New) The method of Claim 125, wherein the genetic information monitors the presence of the biological entity.